

6

Sequences producing significant alignments:			Score (bits)	E Value	
gi 1438904 qb AAC50623.1 	5-HT4L receptor >gi 2494993 sp Q1...	410	e-113	G	
gi 32481997 qb AAP84351.1 	neuropeptide Y receptor Y5 [Homo...	389	e-107	G	
gi 11875770 qb AAG40773.1 	neuropeptide Y receptor Y5 [Maca...	389	e-107		
gi 14029710 qb AAK52800.1 	NPY receptor 5 [Cavia porcellus]	380	e-104		
gi 50978824 ref NP_001003118.1 	neuropeptide Y receptor typ...	379	e-104	G	
gi 1438906 qb AAC52677.1 	5-HT4L receptor >gi 2494994 sp Q6...	364	2e-99	G	
gi 4249729 qb AAD13778.1 	neuropeptide Y5 receptor [Sus scr...	360	3e-98		
gi 6981284 ref NP_037001.1 	neuropeptide Y receptor Y5; Neu...	360	3e-98	G	
gi 2564651 qb AAB81829.1 	neuropeptide Y Y5 receptor [Mus m...	350	3e-95	G	
gi 7710072 ref NP_057917.1 	neuropeptide Y receptor Y5 [Mus...	350	3e-95	G	
gi 3169285 qb AAC17839.1 	neuropeptide Y receptor type 5 [M...	348	1e-94	G	
gi 50746172 ref XP_420388.1 	PREDICTED: similar to neuropep...	281	2e-74	G	
gi 19548984 qb AAK83556.1 	neuropeptide Y receptor Y5 [Gall...	271	3e-71		
gi 33302263 qb AAO62565.1 	NPY receptor Y1 [Squalus acanthias]	116	5e-57		
gi 19548986 qb AAK83557.1 	neuropeptide Y receptor Y1 [Gall...	118	3e-55		
gi 33302259 qb AAO62564.1 	NPY receptor Y6 [Squalus acanthias]	108	2e-53		
gi 2134119 pir S71152	neuropeptide Y/peptide YY receptor Y...	114	3e-53	G	
gi 50746252 ref XP_426285.1 	PREDICTED: similar to neuropep...	118	5e-53	G	
gi 47523648 ref NP_999453.1 	neuropeptide Y Y1 receptor [Su...	118	5e-52	G	

gi 6457648 gb AAD13776.2	neuropeptide Y1 receptor [Sus scr...	118	5e-52	G
gi 18859127 ref NP_571515.1	neuropeptide Y/peptide YY rece...	124	9e-52	G
gi 50950123 ref NP_001002930.1	neuropeptide Y receptor Y1 ...	116	3e-51	G
gi 4505445 ref NP_000900.1	neuropeptide Y receptor Y1 [Hom...	114	1e-50	G
gi 11875766 gb AAG40771.1	neuropeptide Y receptor Y1 [Maca...	114	1e-50	
gi 5410446 gb AAD43060.1	neuropeptide Y receptor Y1 [Cavia...	115	2e-50	
gi 34877858 ref XP_344503.1	neuropeptide Y receptor Y1 [Ra...	116	4e-50	G
gi 189154 gb AAA59920.1	neuropeptide y receptor	112	6e-50	G
gi 57637 emb CAA77579.1	NPY-1 receptor [Rattus rattus] >gi...	115	8e-50	G
gi 111640 pir S12863	G protein-coupled receptor FC5 - rat ...	115	8e-50	
gi 30410856 gb AAH51420.1	Npylr protein [Mus musculus] >gi...	114	1e-49	G
gi 4106397 gb AAD02833.1	neuropeptide Y/peptide YY recepto...	102	1e-45	
gi 6754884 ref NP_035065.1	neuropeptide Y receptor Y6 [Mus...	105	1e-45	G
gi 18253297 gb AAL66410.1	NPY receptor [Lampetra fluviatilis]	118	3e-44	
gi 33302257 gb AAO62563.1	NPY receptor Y4 [Squalus acanthias]	114	2e-43	
gi 19071213 gb AAL84161.1	neuropeptide Y receptor 4 [Gallu...	108	5e-43	
gi 37778942 gb AAN78328.1	neuropeptide Y receptor Y6 [Peca...	100	2e-42	
gi 50746142 ref XP_420373.1	PREDICTED: similar to neuropep...	112	3e-40	G
gi 11545537 gb AAG37898.1	neuropeptide Y receptor Y2 [Gall...	112	3e-40	
gi 49456855 emb CAG46748.1	PPYR1 [Homo sapiens]	113	5e-40	G
gi 46410163 gb AAS93941.1	NPY receptor Y7 [Danio rerio]	112	5e-40	
gi 50749562 ref XP_426511.1	PREDICTED: similar to neuropep...	97	1e-39	G
gi 47217601 emb CAG02528.1	unnamed protein product [Tetrao...	94	2e-39	
gi 18859129 ref NP_571511.1	neuropeptide Y/peptide YY rece...	105	3e-39	G
gi 7417238 gb AAF62507.1	neuropeptide Y-family receptor Y4...	111	4e-39	G
gi 4235257 gb AAD13143.1	neuropeptide Y receptor type 2 [C...	111	5e-39	
gi 51452114 gb AAH75053.2	Neuropeptide Y receptor Y2 [Homo...	111	7e-39	G
gi 961480 dbj BAA09888.1	neuropeptide Y-Y1beta receptor [M...	114	7e-39	G
gi 1314330 gb AAB07760.1	neuropeptide y/peptide YY recepto...	110	1e-38	G
gi 6679122 ref NP_032757.1	neuropeptide Y receptor Y2; NPY...	111	1e-38	G
gi 26340626 dbj BAC33975.1	unnamed protein product [Mus mu...	111	1e-38	G
gi 50755049 ref XP_414599.1	PREDICTED: similar to NPY rece...	117	2e-38	G
gi 13027422 ref NP_076458.1	neuropeptide Y receptor Y2; ne...	110	2e-38	G
gi 1000751 gb AAA93170.1	type 2 neuropeptide Y receptor	109	2e-38	G
gi 4249727 gb AAD13777.1	neuropeptide Y2 receptor [Sus scr...	112	3e-38	
gi 27806023 ref NP_776826.1	neuropeptide Y receptor Y2 [Bo...	110	3e-38	G
gi 13928788 ref NP_113769.1	pancreatic polypeptide recepto...	112	3e-38	G
gi 1109769 emb CAA92322.1	pancreatic polypeptide receptor ...	112	3e-38	G
gi 47523392 ref NP_999315.1	neuropeptide Y Y2 receptor [Su...	111	3e-38	G
gi 11875768 gb AAG40772.1	neuropeptide Y receptor Y2 [Maca...	110	4e-38	
gi 4098212 gb AAD00248.1	neuropeptide Y receptor type 2 [H...	111	1e-37	G
gi 4235259 gb AAD13144.1	pancreatic polypeptide receptor Y...	105	2e-37	
gi 18859131 ref NP_571512.1	neuropeptide Y/peptide YY rece...	105	6e-37	G
gi 47228590 emb CAG05410.1	unnamed protein product [Tetrao...	100	5e-36	
gi 4758474 ref NP_004239.1	G protein-coupled receptor 10; ...	100	2e-35	G
gi 31239533 ref XP_320180.1	ENSANGP00000011806 [Anopheles ...	98	4e-35	G
gi 47223673 emb CAF99282.1	unnamed protein product [Tetrao...	92	2e-34	
gi 1002739 gb AAC50504.1	GPR10	94	3e-33	G
gi 50749931 ref XP_426542.1	PREDICTED: similar to Prolacti...	92	8e-33	G

gi 47228890 emb CAG09405.1 	unnamed protein product [Tetrao...	110	1e-32	
gi 31208067 ref XP_313000.1 	ENSANGP00000020441 [Anopheles ...	88	2e-30	G
gi 17945440 gb AAL48774.1 	RE18294p [Drosophila melanogaster]	91	8e-30	
gi 28571531 ref NP_524245.3 	CG1147-PA [Drosophila melanoga...	91	8e-30	G
gi 13937102 gb AAK50050.1 	neuropeptide F receptor [Drosoph...	91	8e-30	
gi 38087207 ref XP_142008.2 	similar to G protein-coupled r...	105	1e-29	G
gi 34880717 ref XP_231463.2 	similar to G protein-coupled r...	106	3e-29	G
gi 50745619 ref XP_426254.1 	PREDICTED: similar to G protei...	93	1e-28	G
gi 1679632 gb AAB19187.1 	truncated pancreatic polypeptide ...	100	2e-28	
gi 50731261 ref XP_425651.1 	PREDICTED: similar to G protei...	96	2e-28	G
gi 1731790 dbj BAA13103.1 	Y6 encoding protein [Homo sapiens]	100	4e-28	
gi 1857635 gb AAD11810.1 	lymnokinin receptor [Lymnaea stag...	97	2e-27	
gi 5420385 emb CAA57620.1 	G protein-coupled receptor 105 [...	83	4e-27	
gi 85080 pir A41738	neuropeptide Y receptor - fruit fly (D...	94	4e-27	
gi 24643096 ref NP_523404.2 	CG6857-PA [Drosophila melanoga...	106	7e-27	G
gi 51092236 gb AAT94531.1 	AT16733p [Drosophila melanogaster]	93	7e-27	
gi 45549233 ref NP_524525.3 	CG5811-PA [Drosophila melanoga...	93	7e-27	G
gi 25152230 ref NP_509725.2 	neuropeptide receptor NPR1 (46...	77	7e-27	G
gi 7959347 dbj BAA96064.1 	KIAA1540 protein [Homo sapiens]	97	2e-26	G
gi 45768492 gb AAH67473.1 	G protein-coupled receptor 83 [H...	97	2e-26	G
gi 33354257 ref NP_057624.2 	G protein-coupled receptor 83;...	97	2e-26	G
gi 7248882 gb AAF43705.1 	orphan G-protein coupled receptor...	97	2e-26	G
gi 50978808 ref NP_001003108.1 	glucocorticoid induced rece...	97	2e-26	G
gi 34860282 ref XP_346816.1 	hypothetical protein XP_346815...	96	6e-26	G
gi 14028711 gb AAK52473.1 	allatostatin receptor [Periplane...	88	8e-26	
gi 25388079 pir JC7677	allatostatin receptor - American co...	88	8e-26	
gi 2707338 gb AAB92258.1 	cardioexcitatory receptor [Lymnae...	78	8e-26	
gi 45767703 gb AAH67474.1 	G protein-coupled receptor 83 [H...	94	1e-25	G
gi 48139558 ref XP_397024.1 	similar to allatostatin recept...	93	1e-25	G
gi 14279167 gb AAK58514.1 	G-protein-coupled receptor 74 [M...	96	1e-25	G
gi 6753988 ref NP_034417.1 	G protein-coupled receptor 83; ...	94	1e-25	G
gi 45383432 ref NP_989693.1 	neuropeptide FF 1, RFamide-rel...	98	1e-25	G

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|1438904|gb|AAC50623.1|](#) **G** 5-HT4L receptor
[gi|2494993|sp|Q15761|NY5R_HUMAN](#) **G** Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (NPYY5)
Length = 455

Score = 410 bits (1054), Expect = e-113

Identities = 212/263 (80%), Positives = 227/263 (86%), Gaps = 7/263 (2%)

Frame = +2

Query: 17 MSFYSKQDYNMDLELDEYYNKTLATENNTAATRN SDFPVWDDYKSSVDDLQYFLIGLYTF 196
MSFYSKQDYNMDLELDEYYNKTLATENNTAATRN SDFPVWDDYKSSVDDLQYFLIGLYTF
Sbjct: 1 MSFYSKQDYNMDLELDEYYNKTLATENNTAATRN SDFPVWDDYKSSVDDLQYFLIGLYTF 60

Query: 197 VSLLGFMGNLLILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSLVLLDQWMFG 376
 VSLLGFMGNLLILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSLVLLDQWMFG
 Sbjct: 61 VSLLGFMGNLLILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSLVLLDQWMFG 120

Query: 377 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 556
 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI
 Sbjct: 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAI 180

Query: 557 CSPLPVFHSVLVELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLS 724
 CSPLPVFHSVLVELQETFGSALL++ + S + I + LL + L++S
 Sbjct: 181 CSPLPVFHSVLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVS 240

Query: 725 Y---CKSYKCLHTPKKEKQHDGQ 784
 + C+S C + K+ + + +
 Sbjct: 241 HTSVCRSISCGLSNKENRLEENE 263

Score = 172 bits (437), Expect = 1e-41
 Identities = 80/80 (100%), Positives = 80/80 (100%)
 Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
 Sbjct: 376 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 435

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
 GFLNNGIKADLVSLIHCLHM
 Sbjct: 436 GFLNNGIKADLVSLIHCLHM 455

Score = 60.5 bits (145), Expect(2) = 2e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
 ++ SSRYLCVESWPSDSYRIAFTISLLLVQ P
 Sbjct: 200 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 233

Score = 35.0 bits (79), Expect(2) = 2e-12
 Identities = 15/15 (100%), Positives = 15/15 (100%)
 Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749
 ILPLVCLTVSHTSVC
 Sbjct: 231 ILPLVCLTVSHTSVC 245

☐ >gi|32481997|gb|AAP84351.1| ☒ neuropeptide Y receptor Y5 [Homo sapiens]
 gi|5453796|ref|NP_006165.1| ☒ neuropeptide Y receptor Y5 [Homo sapiens]
 gi|27502796|gb|AAH42416.1| ☒ Neuropeptide Y receptor Y5 [Homo sapiens]
 gi|1945449|gb|AAC51295.1| ☒ neuropeptide Y5 receptor [Homo sapiens]
 gi|1620656|gb|AAC50741.1| ☒ neuropeptide Y5 receptor
 Length = 445

Score = 389 bits (999), Expect = e-107
 Identities = 202/253 (79%), Positives = 217/253 (85%), Gaps = 7/253 (2%)
 Frame = +2

Query: 47 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL 226
 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL
 Sbjct: 1 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL 60

Query: 227 LILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
 LILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
 Sbjct: 61 LILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHS 586
 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHS
 Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHS 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
 VELQETFGSALL++ + S + I + LL + L++S+ C+S C
 Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
 + K+ + + +
 Sbjct: 241 GLSNKENRLEENE 253

Score = 172 bits (437), Expect = 1e-41
 Identities = 80/80 (100%), Positives = 80/80 (100%)
 Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
 Sbjct: 366 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
 GFLNNGIKADLVSLIHCLHM
 Sbjct: 426 GFLNNGIKADLVSLIHCLHM 445

Score = 60.5 bits (145), Expect(2) = 2e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQVQLFCP 714
 ++ SSRYLCVESWPSDSYRIAFTISLLLQV P
 Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQVYILP 223

Score = 35.0 bits (79), Expect(2) = 2e-12
 Identities = 15/15 (100%), Positives = 15/15 (100%)
 Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749
 ILPLVCLTVSHTSVC
 Sbjct: 221 ILPLVCLTVSHTSVC 235

☐ >gi|11875770|gb|AAG40773.1| neuropeptide Y receptor Y5 [Macaca mulatta]
Length = 445

Score = 389 bits (999), Expect = e-107
Identities = 202/253 (79%), Positives = 217/253 (85%), Gaps = 7/253 (2%)
Frame = +2

Query: 47 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
Sbjct: 1 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPTLTSLVLLDQWMFGKVMCHIMPFL 406
LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPTLTSLVLLDQWMFGKVMCHIMPFL
Sbjct: 61 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPTLTSLVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHS 586
QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHS
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHS 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
VELQETFGSALL++ + S + I + LL + L++S+ C+S C
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
+ K+ + + +
Sbjct: 241 GLSNKENRLEENE 253

Score = 171 bits (434), Expect = 2e-41
Identities = 79/80 (98%), Positives = 80/80 (100%)
Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 366 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
GFLNNGIKADL+SLIHCLHM
Sbjct: 426 GFLNNGIKADLMSLIHCLHM 445

Score = 60.5 bits (145), Expect(2) = 2e-12
Identities = 28/34 (82%), Positives = 30/34 (88%)
Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLQVLCF 714
++ SSRYLCVESWPSDSYRIAFTISLLLQV P
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 223

Score = 35.0 bits (79), Expect(2) = 2e-12
Identities = 15/15 (100%), Positives = 15/15 (100%)
Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749
ILPLVCLTVSHTSVC

Sbjct: 221 ILPLVCLTVSHTSVC 235

☐ >gi|14029710|qb|AAK52800.1| NPY receptor 5 [Cavia porcellus]
Length = 446

Score = 380 bits (977), Expect = e-104
Identities = 197/253 (77%), Positives = 214/253 (84%), Gaps = 7/253 (2%)
Frame = +2

Query: 47 MDLELDEYYNKTLATENNTAATRNDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
MDLEL EYYNKTLATENNT TRNSDFPVWDDY+SSVDDLQYFLIGLYTFVSLLGFMGNL
Sbjct: 1 MDLELKEYYNKTLATENNTTTTRNSDFPVWDDYRSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
LILMAL+KKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
Sbjct: 61 LILMALIKKRQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586
QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
VELQETFGSALL++ + S + I + LL + L++S+ C+S C
Sbjct: 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
+ K+ + + +
Sbjct: 241 GLSNKENRLEENE 253

Score = 170 bits (431), Expect = 5e-41
Identities = 78/80 (97%), Positives = 80/80 (100%)
Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
Sbjct: 366 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
GFLNNGIKADL+SLIHCLH+
Sbjct: 426 GFLNNGIKADLMSLIHCLHL 445

Score = 60.5 bits (145), Expect(2) = 2e-12
Identities = 28/34 (82%), Positives = 30/34 (88%)
Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
++ SSRYLCVESWPSDSYRIAFTISLLLVQ P
Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLVQYILP 223

Score = 35.0 bits (79), Expect(2) = 2e-12
Identities = 15/15 (100%), Positives = 15/15 (100%)
Frame = +3

Query: 705 ILPLVCLTVSHTSVC 749
 ILPLVCLTVSHTSVC
 Sbjct: 221 ILPLVCLTVSHTSVC 235

☐ >gi|50978824|ref|NP_001003118.1| ☒ G neuropeptide Y receptor type 5 [Canis familia
 gi|3169283|gb|AAC17838.1| ☒ G neuropeptide Y receptor type 5 [Canis familiaris]
 gi|3914178|sp|O62729|NY5R_CANFA Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 r
 receptor) (NPYY5)
 Length = 446

Score = 379 bits (973), Expect = e-104
 Identities = 197/253 (77%), Positives = 214/253 (84%), Gaps = 7/253 (2%)
 Frame = +2

Query: 47 MDLELDEYYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 226
 MDLEL ++YNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL
 Sbjct: 1 MDLELQDFYNKTLATENNTAATRNSDFPVWDDYKSSVDDLQYFLIGLYTFVSLLGFMGNL 60

Query: 227 LILMALMKKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 406
 LILMALM+KRNQKT VNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL
 Sbjct: 61 LILMALMRKRNQKTMVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHIMPFL 120

Query: 407 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 586
 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL
 Sbjct: 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVWTLGFAICSPLPVFHSL 180

Query: 587 VELQETFGSALLAAGIYVL----SHGHLIHTELPLLSLYC*FSYSALSLSY---CKSYKC 745
 VELQETF SALL++ + S + I + LL + L++S+ C+S C
 Sbjct: 181 VELQETFDSALLSSRYLCVESWPSDSYRIAFTISLLLVQYILPLVCLTVSHTSVCRSISC 240

Query: 746 LHTPKKEKQHDGQ 784
 + K+ K + +
 Sbjct: 241 GLSNKENKLEENE 253

Score = 169 bits (428), Expect = 1e-40
 Identities = 78/80 (97%), Positives = 79/80 (98%)
 Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 1004
 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY
 Sbjct: 366 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLLGMMSCCLNPILY 425

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064
 GFLNNGIKADL+SLI CLHM
 Sbjct: 426 GFLNNGIKADLISLIQCLHM 445

Score = 60.5 bits (145), Expect(2) = 1e-12
 Identities = 28/34 (82%), Positives = 30/34 (88%)
 Frame = +1

Query: 613 SIASSRYLCVESWPSDSYRIAFTISLLLVQLFCP 714
 ++ SSRYLCVESWPSDSYRIAFTISLLLVQ P

Sbjct: 190 ALLSSRYLCVESWPSDSYRIAFTISLLLQYILP 223

Score = 36.2 bits (82), Expect(2) = 1e-12
 Identities = 18/33 (54%), Positives = 24/33 (72%), Gaps = 1/33 (3%)
 Frame = +3

Query: 705 ILPLVCLTVSHTSVCIRLK-RRNNMMDKMRDNK 800

ILPLVCLTVSHTSVC + +N +K+ +N+

Sbjct: 221 ILPLVCLTVSHTSVCRSISCGLSNKENKLEENE 253

☐ >gi|1438906|gb|AAC52677.1| ☒ 5-HT4L receptor

gi|2494994|sp|Q63634|NY5R RAT ☒ Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 r
 receptor)
 Length = 456

Score = 364 bits (934), Expect = 2e-99
 Identities = 186/257 (72%), Positives = 212/257 (82%), Gaps = 7/257 (2%)
 Frame = +2

Query: 35 QDYNMDLELDEYYNKTATENNTAATRNSTDFPVWDDYKSSVDDLQYFLIGLYTFVSLLG 214

QD +M+ +L+E++NKT TENNTAA RN+ FP W+DY+ SVDDLQYFLIGLYTFVSLLG

Sbjct: 8 QDSSMEFKLEEHNKTFVTENNTAAARNAAFPWEDYRGSVDDLQYFLIGLYTFVSLLG 67

Query: 215 MGNNLILMALMKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKVMCHI 394

MGNNLILMA+MKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGK MCHI

Sbjct: 68 MGNNLILMAVMKRNQKTTVNFLIGNLAFSDILVVLFCSPFTLTSVLLDQWMFGKAMCHI 127

Query: 395 MPFLQCVSVLVSTLILISIAIVRYHMIKHPISSNNLTANHGYFLIATVWTLGFAICSPLPV 574

MPFLQCVSVLVSTLILISIAIVRYHMIKHPISSNNLTANHGYFLIATVWTLGFAICSPLPV

Sbjct: 128 MPFLQCVSVLVSTLILISIAIVRYHMIKHPISSNNLTANHGYFLIATVWTLGFAICSPLPV 187

Query: 575 FHSLVELQETFGSALLAAGIYVL----SHGHLIHTEPLLSLYC*FSYSALSLSY---CK 733

FHSLVEL+ETFGSALL++ + S + I + LL + L++S+ C+

Sbjct: 188 FHSLVELKETFGSALLSSKYLCEWPSDSYRIAFTISLLLQYILPLVCLTVSHTSVCR 247

Query: 734 SYKCLHTPKKEKQHDGQ 784

S C + K+ + + +

Sbjct: 248 SISCGLSHKENRLEENE 264

Score = 167 bits (424), Expect = 3e-40
 Identities = 77/80 (96%), Positives = 79/80 (98%)
 Frame = +3

Query: 825 VFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGMMSCCLNPILY 1004

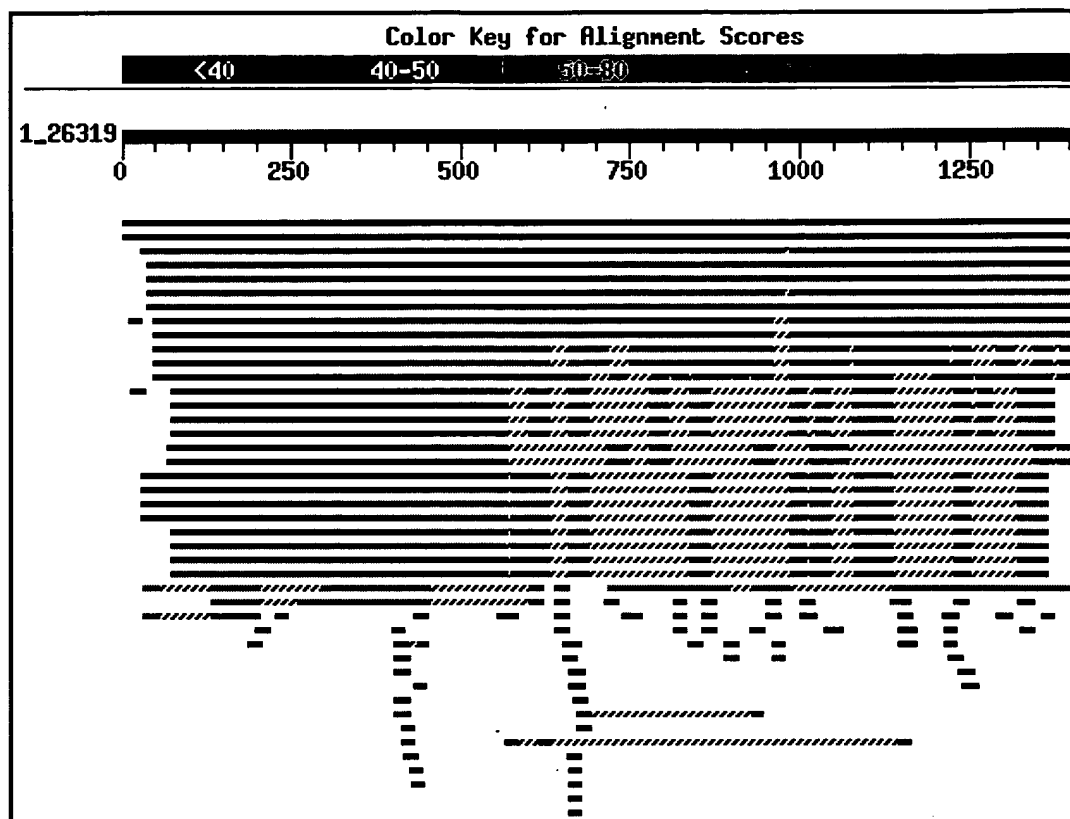
VFYRLTILILVFAVSWMPLH+FHVVTDNDNLISNRHFKLVYCICHLGMMSCCLNPILY

Sbjct: 376 VFYRLTILILVFAVSWMPLHVFHVVTDFNDNLISNRHFKLVYCICHLGMMSCCLNPILY 435

Query: 1005 GFLNNGIKADLVSLIHCLHM 1064

GFLNNGIKADL +LIHCLHM

Sbjct: 436 GFLNNGIKADLRALIHCLHM 455



1406

Sequences producing significant alignments:			Score (bits)	E Value	
gi 16756377 gb AC079238.7 	Homo sapiens BAC clone RP11-719L...		1132	0.0	
gi 1438903 gb U56079.1 HSU56079	Human Y5 receptor mRNA, com...		1132	0.0	GIU
gi 1620655 gb U66275.1 HSU66275	Human neuropeptide Y5 recep...		1074	0.0	GIU
gi 22832895 gb BC034224.1 	Homo sapiens neuropeptide Y rece...		1059	0.0	GIU
gi 31377784 ref NM_006174.2 	Homo sapiens neuropeptide Y re...		1059	0.0	GIU E
gi 27502795 gb BC042416.1 	Homo sapiens neuropeptide Y rece...		1059	0.0	GIU
gi 1945448 gb U94320.1 HSU94320	Human neuropeptide Y5 recep...		1059	0.0	GIU E
gi 32481996 gb AY322538.1 	Homo sapiens neuropeptide Y rece...		1041	0.0	G
gi 11875769 gb AF303091.1 AF303091	Macaca mulatta neuropept...		969	0.0	
gi 50978823 ref NM_001003118.1 	Canis familiaris neuroepti...		779	0.0	GIU
gi 3169282 gb AF049328.1 AF049328	Canis familiaris neuroep...		779	0.0	GIU E
gi 14029709 gb AF363240.1 AF363240	Cavia porcellus NPY rece...		660	0.0	
gi 6981283 ref NM_012869.1 	Rattus norvegicus neuropeptide ...		545	e-152	GIU E
gi 1620657 gb U66274.1 RNU66274	Rattus norvegicus neuroept...		545	e-152	GIU E
gi 1438905 gb U56078.1 RNU56078	Rattus norvegicus Y5 recept...		545	e-152	GIU
gi 3098509 gb AF044264.1 AF044264	Rattus norvegicus neurope...		545	e-152	GIU
gi 4249728 gb AF106083.1 AF106083	Sus scrofa neuropeptide Y...		539	e-150	
gi 3808059 dbj AB019185.1 	Sus scrofa NPY Y5 gene for neuro...		539	e-150	
gi 22476189 gb AC123796.2 	Mus musculus BAC clone RP24-320P...		523	e-145	
gi 33942177 gb AC116731.9 	Mus musculus chromosome 8, clone...		523	e-145	
gi 52839799 gb AC100541.17 	Mus musculus chromosome 8, clon...		523	e-145	
gi 2564650 gb AF022948.1 AF022948	Mus musculus neuropeptide...		523	e-145	G

gi 26337480 dbj AK045587.1 	Mus musculus adult male corpora...	523	e-145	G U
gi 3169284 gb AF049329.1 AF049329	Mus musculus neuropeptide...	519	e-144	G U E
gi 7710071 ref NM_016708.1 	Mus musculus neuropeptide Y rec...	515	e-143	G U E
gi 6714644 dbj AB001346.1 	Mus musculus mRNA for neuropepti...	515	e-143	G U E
gi 50746171 ref XM_420388.1 	PREDICTED: Gallus gallus simil...	98	7e-17	G
gi 19548983 gb AY040844.1 	Gallus gallus neuropeptide Y rec...	92	4e-15	
gi 976208 gb L47169.1 HUMNPYAC	Homo sapiens neuropeptide Y ...	70	2e-08	
gi 46427829 emb CR389184.1 	Gallus gallus finished cDNA, cl...	56	2e-04	U
gi 51100952 dbj AB104827.2 	Candida boidinii FGH1 gene for ...	44	0.87	
gi 31746714 gb AC133101.4 	Mus musculus BAC clone RP23-154M...	42	3.5	
gi 37693674 gb AC121082.13 	Mus musculus chromosome 7, clon...	42	3.5	
gi 32880270 gb AC118695.10 	Mus musculus chromosome 19, clo...	42	3.5	
gi 53379715 gb AC149588.4 	Mus musculus chromosome 15 clone...	42	3.5	
gi 52077841 gb AC132394.3 	Mus musculus chromosome 6 clone ...	42	3.5	
gi 16603965 gb AC076968.38 	Homo sapiens 12 BAC RP11-686F15...	42	3.5	
gi 48675465 gb AC132104.3 	Mus musculus BAC clone RP24-364N...	42	3.5	
gi 34536220 dbj AK128706.1 	Homo sapiens cDNA FLJ46873 fis,...	42	3.5	U
gi 49170190 gb AC124958.13 	Medicago truncatula clone mth2-...	42	3.5	
gi 21955079 gb AC104016.8 	Homo sapiens chromosome 11, clon...	42	3.5	
gi 20334476 gb AC079822.13 	Homo sapiens 3 BAC RP11-413G22 ...	42	3.5	
gi 22549646 gb AC092964.8 	Homo sapiens 3 BAC RP11-423E7 (R...	42	3.5	
gi 20986479 gb AC084701.5 	Homo sapiens chromosome 18, clon...	42	3.5	
gi 2462139 emb Z70681.1 CEC30F2	Caenorhabditis elegans cosm...	42	3.5	
gi 28173126 gb AC100865.5 	Homo sapiens chromosome 11, clon...	42	3.5	
gi 27884981 gb AC117539.6 	Papio hamadryas, clone RP41-208E...	42	3.5	
gi 15638824 gb AC096569.1 	Homo sapiens BAC clone RP11-347B...	42	3.5	
gi 14702085 gb AC013722.8 	Homo sapiens BAC clone RP11-299H...	42	3.5	
gi 15431133 gb AC013660.9 	Homo sapiens, clone RP11-20A14, ...	42	3.5	
gi 2109298 gb AF000132.1 AHAF000132	Amaranthus hypochondria...	42	3.5	
gi 13560010 emb AL356318.7 	Human DNA sequence from clone R...	42	3.5	
gi 24366576 emb AL808118.8 	Mouse DNA sequence from clone R...	42	3.5	
gi 10280826 gb AC012531.11 AC012531	Homo sapiens, clone RP1...	42	3.5	
gi 42491502 gb AC102734.11 	Mus musculus chromosome 6, clon...	42	3.5	
gi 608510 gb U16311.1 BRU16311	Brachydanio rerio homeodomai...	42	3.5	G U
gi 26330583 dbj AK035302.1 	Mus musculus adult male urinary...	42	3.5	G U
gi 26084230 dbj AK034836.1 	Mus musculus 12 days embryo emb...	42	3.5	G U
gi 21211711 emb AL359771.27 	Human DNA sequence from clone ...	42	3.5	
gi 38678612 gb AC117702.10 	Mus musculus chromosome 10, clo...	40	14	
gi 17570664 ref NM_077495.1 	Caenorhabditis elegans allatos...	40	14	G
gi 28604212 gb AC124775.4 	Mus musculus BAC clone RP23-60N3...	40	14	
gi 19310330 gb AC104789.4 	Homo sapiens BAC clone RP11-138B...	40	14	
gi 48391178 gb AY584422.1 	Xantusia bezyi isolate Xbe5_Pin5...	40	14	
gi 48391102 gb AY584384.1 	Xantusia bezyi isolate Xbe2_GaL1...	40	14	
gi 34368596 gb AC120736.4 	Rattus norvegicus 11 BAC CH230-2...	40	14	
gi 33242564 gb AY336522.1 	Sulfolobus solfataricus strain P...	40	14	
gi 44844336 emb BX247953.2 	Mouse DNA sequence from clone R...	40	14	
gi 30725969 gb AC100271.6 	Mus musculus, clone RP23-77E14, ...	40	14	
gi 51233561 gb AC110499.19 	Mus musculus chromosome 1, clon...	40	14	
gi 51036712 gb AC130808.26 	Medicago truncatula clone mth2-...	40	14	
gi 50761406 ref XM_424720.1 	PREDICTED: Gallus gallus simil...	40	14	G
gi 20258986 gb AY091270.1 	Arabidopsis thaliana putative si...	40	14	G U
gi 17380917 gb AY063915.1 	Arabidopsis thaliana putative pu...	40	14	G U
gi 48675548 gb AC134472.4 	Mus musculus BAC clone RP23-123E...	40	14	
gi 46195482 gb AC135316.15 	Medicago truncatula clone mth2-...	40	14	
gi 22539131 gb AC105009.13 	Homo sapiens chromosome 8, clon...	40	14	

gi 21909528 gb AC105235.7 	Homo sapiens chromosome 8, clone...	40	14
gi 34786898 emb AL831812.5 CNS08CAP	Oryza sativa chromosome...	40	14
gi 21535755 emb AL713907.3 CNS07YQ7	Oryza sativa chromosome...	40	14
gi 10944453 gb AC008752.6 	Homo sapiens chromosome 19 clone...	40	14
gi 33620400 emb AL929018.14 	Mouse DNA sequence from clone ...	40	14
gi 21281541 gb AC104163.2 	Homo sapiens chromosome 3 clone ...	40	14
gi 48717527 gb AC122169.23 	Medicago truncatula clone mth2-...	40	14
gi 27228874 gb AC093576.3 	Homo sapiens chromosome 1 clone ...	40	14
gi 49528096 emb CR380958.1 	Candida glabrata strain CBS138 ...	40	14
gi 25137544 dbj AP005900.1 	Homo sapiens genomic DNA, chrom...	40	14
gi 17921243 gb AC022317.8 	Homo sapiens chromosome 4 clone ...	40	14
gi 17985904 gb AC093581.2 	Homo sapiens chromosome 1 clone ...	40	14
gi 17155036 gb AC091819.3 	Homo sapiens chromosome 5 clone ...	40	14
gi 24417223 dbj AP005663.2 	Homo sapiens genomic DNA, chrom...	40	14
gi 13992802 gb AC068551.6 	Homo sapiens BAC clone RP11-720N...	40	14
gi 16554344 gb AC011395.5 	Homo sapiens chromosome 5 clone ...	40	14
gi 46240964 gb AC145942.4 	Gallus gallus chromosome UNK clo...	40	14
gi 11968293 gb AC010368.4 AC010368	Homo sapiens chromosome ...	40	14
gi 47847914 dbj AP004168.3 	Oryza sativa (japonica cultivar...	40	14
gi 12309635 emb AL450428.6 	Human DNA sequence from clone R...	40	14
gi 10441989 gb AF218030.1 AF218030	Homo sapiens clone PP79 ...	40	14
gi 10441953 gb AF218012.1 AF218012	Homo sapiens clone PP379...	40	14
gi 21734414 emb AL833764.1 HSM805077	Homo sapiens mRNA; cDN...	40	14

GIU
GIUE
G

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|16756377|gb|AC079238.7|](#) ☒ Homo sapiens BAC clone RP11-719L21 from 4, complet
Length = 142462

Score = 1132 bits (571), Expect = 0.0
Identities = 571/571 (100%)
Strand = Plus / Plus

```

Query: 1      ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
             |||
Sbjct: 128642 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 128701

Query: 61      cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 120
             |||
Sbjct: 128702 cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 128761

Query: 121     tgattttcccagctctgggatgactataaaagcagtgtagatgacttacagtattttctgat 180
             |||
Sbjct: 128762 tgattttcccagctctgggatgactataaaagcagtgtagatgacttacagtattttctgat 128821

Query: 181     tgggctctatacatTTTgtaagtcttcttggtttatggggaatctacttattttaatggc 240
             |||
Sbjct: 128822 tgggctctatacatTTTgtaagtcttcttggtttatggggaatctacttattttaatggc 128881

```

Query: 241 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300
|||||
Sbjct: 128882 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 128941

Query: 301 ttctgatatcttggttggtgctgttttgctcacctttcacactgacgtctgtcttgctgga 360
|||||
Sbjct: 128942 ttctgatatcttggttggtgctgttttgctcacctttcacactgacgtctgtcttgctgga 129001

Query: 361 tcagtggatgtttgcaaagtcagtgtccatattatgccttttcttcaatgtgtgtcagt 420
|||||
Sbjct: 129002 tcagtggatgtttgcaaagtcagtgtccatattatgccttttcttcaatgtgtgtcagt 129061

Query: 421 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaaca 480
|||||
Sbjct: 129062 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaaca 129121

Query: 481 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 540
|||||
Sbjct: 129122 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 129181

Query: 541 actaggttttgccatctgttctcccttcca 571
|||||
Sbjct: 129182 actaggttttgccatctgttctcccttcca 129212

Score = 69.9 bits (35), Expect = 2e-08
Identities = 35/35 (100%)
Strand = Plus / Plus

Query: 810 cagatgttcatgaattgagagtaaaacgttctgtt 844
|||||
Sbjct: 129721 cagatgttcatgaattgagagtaaaacgttctgtt 129755

Score = 65.9 bits (33), Expect = 2e-07
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 1254 ttctgttacaagaataaaaaagagatctcgaag 1286
|||||
Sbjct: 129749 ttctgttacaagaataaaaaagagatctcgaag 129781

Score = 63.9 bits (32), Expect = 9e-07
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 1346 tgatgtcctgttggtcttaatccaattctatat 1377

|||||
 Sbjct: 129931 tgatgtcctgttgtcttaatccaattctatat 129962

Score = 63.9 bits (32), Expect = 9e-07
 Identities = 32/32 (100%)
 Strand = Plus / Plus

Query: 1316 acaatcttattttcaaataaggcatttcaagttg 1347
 |||||
 Sbjct: 129871 acaatcttattttcaaataaggcatttcaagttg 129902

Score = 63.9 bits (32), Expect = 9e-07
 Identities = 32/32 (100%)
 Strand = Plus / Plus

Query: 719 cacagaagaagatatagcaagaagacagcatg 750
 |||||
 Sbjct: 129540 cacagaagaagatatagcaagaagacagcatg 129571

Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus

Query: 1376 atttagtgcccttatacactgtcttcatat 1406
 |||||
 Sbjct: 129991 atttagtgcccttatacactgtcttcatat 130021

Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus

Query: 1287 agtatttgctgttagttggatgccactacac 1317
 |||||
 Sbjct: 129812 agtatttgctgttagttggatgccactacac 129842

Score = 61.9 bits (31), Expect = 4e-06
 Identities = 31/31 (100%)
 Strand = Plus / Plus

Query: 1226 cttgctttgagataaaacctgaagaaaattc 1256
 |||||
 Sbjct: 129691 cttgctttgagataaaacctgaagaaaattc 129721

Score = 61.9 bits (31), Expect = 4e-06
Identities = 31/31 (100%)
Strand = Plus / Plus

Query: 1196 actttggctctgtaagaagtcagctctcttc 1226
|||||
Sbjct: 129631 actttggctctgtaagaagtcagctctcttc 129661

Score = 61.9 bits (31), Expect = 4e-06
Identities = 31/31 (100%)
Strand = Plus / Plus

Query: 1107 caacttaactcttcatccatccaaaaagagt 1137
|||||
Sbjct: 129452 caacttaactcttcatccatccaaaaagagt 129482

Score = 61.9 bits (31), Expect = 4e-06
Identities = 31/31 (100%)
Strand = Plus / Plus

Query: 630 tttgtcttactgtaagtcatacaagtgctctg 660
|||||
Sbjct: 129361 tttgtcttactgtaagtcatacaagtgctctg 129391

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 931 tgggtttcttaataatgggattaaagctga 960
|||||
Sbjct: 129962 tgggtttcttaataatgggattaaagctga 129991

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 901 ggtgtattgcatttgtcatttgttgggcat 930
|||||
Sbjct: 129902 ggtgtattgcatttgtcatttgttgggcat 129931

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 871 ccttttccatgtggtaactgattttaatga 900
 |||
 Sbjct: 129842 ccttttccatgtggtaactgattttaatga 129871

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 841 tgttttctacagactgaccatactgatatt 870
 |||
 Sbjct: 129782 tgttttctacagactgaccatactgatatt 129811

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 781 atccagtaagttcataccaggggtcccccac 810
 |||
 Sbjct: 129662 atccagtaagttcataccaggggtcccccac 129691

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 751 agagaaccactccagaatacttccagaaaa 780
 |||
 Sbjct: 129602 agagaaccactccagaatacttccagaaaa 129631

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 1167 tgtgttacctgctccagaaagaccttctca 1196
 |||
 Sbjct: 129572 tgtgttacctgctccagaaagaccttctca 129601

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 1137 taaatggagttattcattcatcaaaaaaca 1166
 |||
 Sbjct: 129512 taaatggagttattcattcatcaaaaaaca 129541

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 691 tgggcctcaggtgaaactctctggcagcca 720
|||||
Sbjct: 129482 tgggcctcaggtgaaactctctggcagcca 129511

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 661 agaaaacagacttgaagaaaatgagatgat 690
|||||
Sbjct: 129422 agaaaacagacttgaagaaaatgagatgat 129451

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1077 cagaagtataagctgtggattgtccaacaa 1106
|||||
Sbjct: 129392 cagaagtataagctgtggattgtccaacaa 129421

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1047 attgctagttcagtatattctgcccttagt 1076
|||||
Sbjct: 129332 attgctagttcagtatattctgcccttagt 129361

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 601 ttcatacagaattgcctttactatctcttt 630
|||||
Sbjct: 129302 ttcatacagaattgcctttactatctcttt 129331

Score = 60.0 bits (30), Expect = 1e-05
Identities = 30/30 (100%)
Strand = Plus / Plus

Query: 1017 gtatttatgtgttgagtcattggccatctga 1046
 |||
 Sbjct: 129272 gtatttatgtgttgagtcattggccatctga 129301

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 571 aacatttggttcagcattgctgagcagcag 600
 |||
 Sbjct: 129242 aacatttggttcagcattgctgagcagcag 129271

Score = 60.0 bits (30), Expect = 1e-05
 Identities = 30/30 (100%)
 Strand = Plus / Plus

Query: 987 agtgtttcacagtcttgtggaacttcaaga 1016
 |||
 Sbjct: 129212 agtgtttcacagtcttgtggaacttcaaga 129241

Score = 54.0 bits (27), Expect = 0.001
 Identities = 27/27 (100%)
 Strand = Plus / Plus

Query: 961 gtaataattctcactgtttaccaagga 987
 |||
 Sbjct: 130022 gtaataattctcactgtttaccaagga 130048

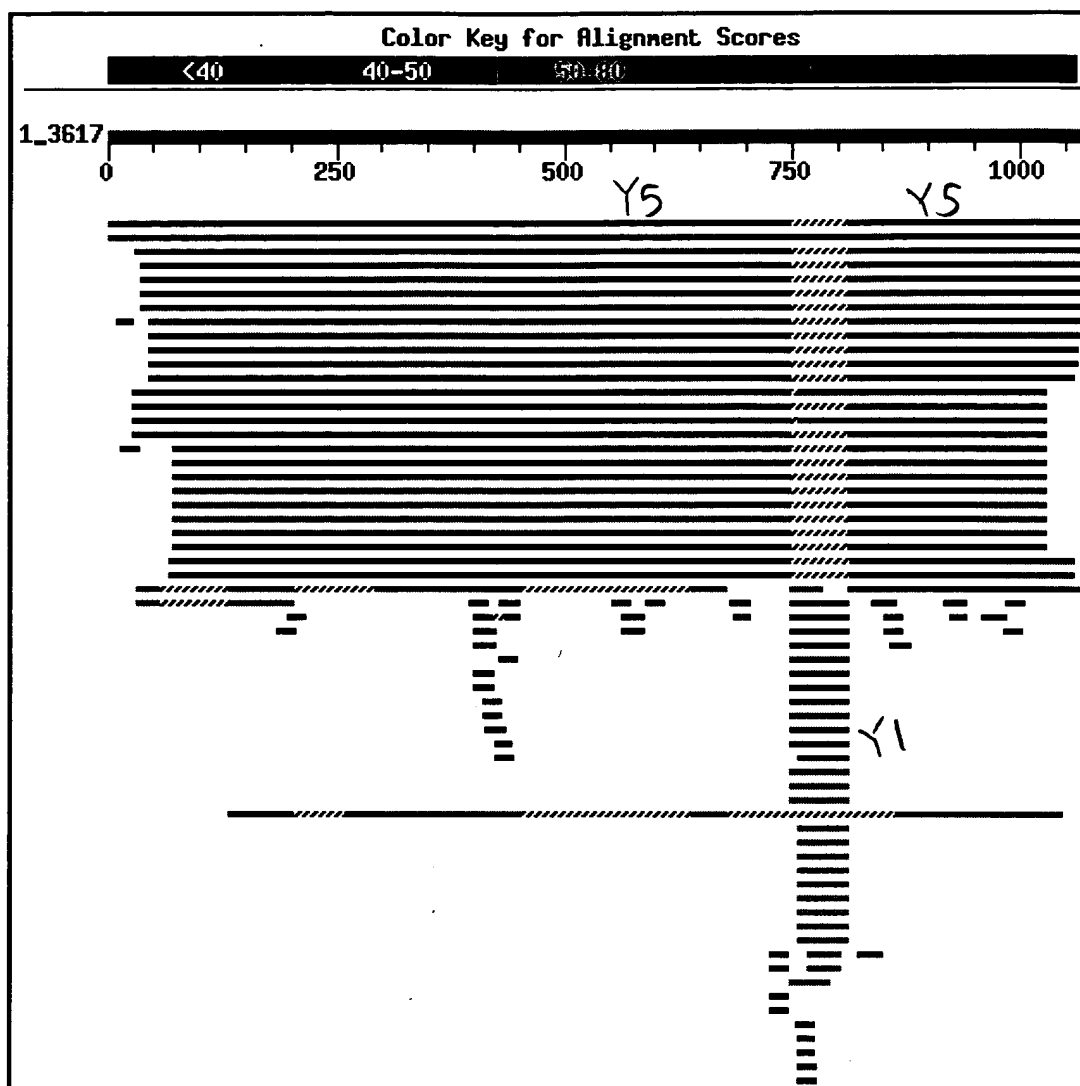
☐ >gi|1438903|gb|U56079.1|HSU56079 **GU** Human Y5 receptor mRNA, complete cds
 Length = 1418

Score = 1132 bits (571), Expect = 0.0
 Identities = 571/571 (100%)
 Strand = Plus / Plus

Query: 1 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
 |||
 Sbjct: 10 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 69

Query: 61 cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 120
 |||
 Sbjct: 70 cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 129

Query: 121 tgatttcccagtcctgggatgactataaaagcagtgtagatgacttacagtattttctgat 180
 |||



Sequences producing significant alignments:			Score (bits)	E Value	
gi 16756377 qb AC079238.7 	Homo sapiens BAC clone RP11-719L...		1459	0.0	
gi 1438903 qb U56079.1 HSU56079	Human Y5 receptor mRNA, com...		1459	0.0	G U
gi 1620655 qb U66275.1 HSU66275	Human neuropeptide Y5 recep...		1402	0.0	G U
gi 22832895 qb BC034224.1 	Homo sapiens neuropeptide Y rece...		1386	0.0	G U
gi 31377784 ref NM_006174.2 	Homo sapiens neuropeptide Y re...		1386	0.0	G U E
gi 27502795 qb BC042416.1 	Homo sapiens neuropeptide Y rece...		1386	0.0	G U
gi 1945448 qb U94320.1 HSU94320	Human neuropeptide Y5 recep...		1386	0.0	G U E
gi 32481996 qb AY322538.1 	Homo sapiens neuropeptide Y rece...		1368	0.0	G
gi 11875769 qb AF303091.1 AF303091	Macaca mulatta neuropept...		1289	0.0	
gi 50978823 ref NM_001003118.1 	Canis familiaris neuropepti...		971	0.0	G U
gi 3169282 qb AF049328.1 AF049328	Canis familiaris neuropep...		971	0.0	G U E
gi 14029709 qb AF363240.1 AF363240	Cavia porcellus NPY rece...		932	0.0	
gi 22476189 qb AC123796.2 	Mus musculus BAC clone RP24-320P...		692	0.0	
gi 33942177 qb AC116731.9 	Mus musculus chromosome 8, clone...		692	0.0	
gi 52839799 qb AC100541.17 	Mus musculus chromosome 8, clon...		692	0.0	

gi 2564650 gb AF022948.1 AF022948	Mus musculus neuropeptide...	692	0.0	G
gi 26337480 dbj AK045587.1 	Mus musculus adult male corpora...	692	0.0	GIU
gi 7710071 ref NM_016708.1 	Mus musculus neuropeptide Y rec...	684	0.0	GIUE
gi 6714644 dbj AB001346.1 	Mus musculus mRNA for neuropepti...	684	0.0	GIUE
gi 3169284 gb AF049329.1 AF049329	Mus musculus neuropeptide...	684	0.0	GIUE
gi 6981283 ref NM_012869.1 	Rattus norvegicus neuropeptide ...	672	0.0	GIUE
gi 1620657 gb U66274.1 RNU66274	Rattus norvegicus neuroept...	672	0.0	GIUE
gi 1438905 gb U56078.1 RNU56078	Rattus norvegicus Y5 recept...	672	0.0	GIU
gi 3098509 gb AF044264.1 AF044264	Rattus norvegicus neuroepe...	672	0.0	GIU
gi 4249728 gb AF106083.1 AF106083	Sus scrofa neuropeptide Y...	668	0.0	
gi 3808059 dbj AB019185.1 	Sus scrofa NPY Y5 gene for neuro...	668	0.0	
gi 976208 gb L47169.1 HUMNPYAC	Homo sapiens neuropeptide Y ...	460	e-126	
gi 41350310 ref NM_000909.4 	Homo sapiens neuropeptide Y re...	125	2e-25	GIU
gi 47939538 gb BC071720.1 	Homo sapiens neuropeptide Y rece...	125	2e-25	GIU
gi 34194271 gb BC036657.2 	Homo sapiens neuropeptide Y rece...	125	2e-25	GIU
gi 45239064 gb AY548168.1 	Homo sapiens neuropeptide Y1 rec...	125	2e-25	GIU
gi 1430810 emb X99269.1 HSNPYY1	H.sapiens NPY1 gene	125	2e-25	G
gi 189155 gb M88461.1 HUMNEYPEPY	Human neuropeptide Y pepti...	125	2e-25	GIUE
gi 189284 gb L07615.1 HUMNPYY1A2	Human neuropeptide Y recep...	125	2e-25	GIUE
gi 189153 gb M84755.1 HUMNEUYREC	Human neuropeptide y recep...	125	2e-25	GIUE
gi 11875765 gb AF303089.1 AF303089	Macaca mulatta neuropept...	117	6e-23	
gi 50950122 ref NM_001002930.1 	Canis familiaris neuropepti...	109	1e-20	GIU
gi 2988393 gb AF005778.1 AF005778	Canis familiaris neuroep...	109	1e-20	GIUE
gi 5410445 gb AF135061.1 AF135061	Cavia porcellus neuropept...	103	8e-19	
gi 50746171 ref XM_420388.1 	PREDICTED: Gallus gallus simil...	98	5e-17	G
gi 47523647 ref NM_214288.1 	Sus scrofa neuropeptide Y Y1 r...	96	2e-16	GIU
gi 6457647 gb AF106081.2 AF106081	Sus scrofa neuropeptide Y...	96	2e-16	G
gi 9789708 gb AF005779.2 AF005779	Sus scrofa neuropeptide Y...	96	2e-16	GIU
gi 19548983 gb AY040844.1 	Gallus gallus neuropeptide Y rec...	92	3e-15	
gi 34877857 ref XM_344502.1 	Rattus norvegicus neuropeptide...	76	2e-10	GIU
gi 30410855 gb BC051420.1 	Mus musculus neuropeptide Y rece...	76	2e-10	GIU
gi 6754881 ref NM_010934.1 	Mus musculus neuropeptide Y rec...	76	2e-10	GIUE
gi 53442 emb Z18283.1 MMNPY1E03	Mus musculus of NPY-1 recep...	76	2e-10	G
gi 57636 emb Z11504.1 RRNPV1R	R.rattus mRNA for NPY-1 receptor	76	2e-10	GE
gi 53438 emb Z18280.1 MMNPY1CDS	Mus musculus NPY-1 receptor	76	2e-10	GE
gi 961479 dbj D63819.1 MUSNYY1RB	Mouse mRNA for neuropeptid...	76	2e-10	GIUE
gi 961477 dbj D63818.1 MUSNYY1RA	Mouse mRNA for neuropeptid...	76	2e-10	GIUE
gi 50746251 ref XM_426285.1 	PREDICTED: Gallus gallus simil...	64	7e-07	G
gi 19548985 gb AY040845.1 	Gallus gallus neuropeptide Y rec...	64	7e-07	
gi 409169 gb L25416.1 XELNPYPYY	Xenopus laevis NPY/PYY rece...	64	7e-07	GIU
gi 46427829 emb CR389184.1 	Gallus gallus finished cDNA, cl...	56	2e-04	U
gi 33302262 gb AY177273.1 AY177272S2	Squalus acanthias NPY ...	56	2e-04	
gi 1480713 gb U62122.1 OAU62122	Ovis aries Y1 neuropeptide ...	56	2e-04	GIU
gi 18425235 gb AC093027.12 	Homo sapiens 12q BAC RP11-701B6...	48	0.042	
gi 51988057 gb AC123647.9 	Mus musculus chromosome 3, clone...	44	0.66	
gi 51100952 dbj AB104827.2 	Candida boidinii FGH1 gene for ...	44	0.66	
gi 31746714 gb AC133101.4 	Mus musculus BAC clone RP23-154M...	42	2.6	
gi 37693674 gb AC121082.13 	Mus musculus chromosome 7, clon...	42	2.6	
gi 53379715 gb AC149588.4 	Mus musculus chromosome 15 clone...	42	2.6	

gi 52077841 gb AC132394.3 	Mus musculus chromosome 6 clone ...	42	2.6	
gi 49533628 gb AC115341.6 	Rattus norvegicus 3 BAC CH230-24...	42	2.6	
gi 20334476 gb AC079822.13 	Homo sapiens 3 BAC RP11-413G22 ...	42	2.6	
gi 20986479 gb AC084701.5 	Homo sapiens chromosome 18, clon...	42	2.6	
gi 2462139 emb Z70681.1 CEC30F2	Caenorhabditis elegans cosm...	42	2.6	
gi 28144384 gb AC008443.10 	Homo sapiens chromosome 5 clone...	42	2.6	
gi 27228882 gb AC104463.3 	Homo sapiens chromosome 1 clone ...	42	2.6	
gi 26080542 gb AC098934.3 	Homo sapiens chromosome 1 clone ...	42	2.6	
gi 4753229 gb AC006335.2 AC006335	Homo sapiens BAC clone RP...	42	2.6	
gi 15431133 gb AC013660.9 	Homo sapiens, clone RP11-20A14, ...	42	2.6	
gi 7408112 gb AC017019.3 AC017019	Homo sapiens BAC clone RP...	42	2.6	
gi 608510 gb U16311.1 BRU16311	Brachydanio rerio homeodomai...	42	2.6	GU
gi 26330583 dbj AK035302.1 	Mus musculus adult male urinary...	42	2.6	GU
gi 26084230 dbj AK034836.1 	Mus musculus 12 days embryo emb...	42	2.6	GU
gi 21655430 emb AL732316.10 	Mouse DNA sequence from clone ...	42	2.6	
gi 38678612 gb AC117702.10 	Mus musculus chromosome 10, clo...	40	10	
gi 17570664 ref NM_077495.1 	Caenorhabditis elegans allatos...	40	10	G
gi 22539392 gb AC114918.4 	Mus musculus BAC clone RP23-86N2...	40	10	
gi 33242564 gb AY336522.1 	Sulfolobus solfataricus strain P...	40	10	
gi 51854744 gb AC133187.3 	Mus musculus chromosome 1 clone ...	40	10	
gi 44844336 emb BX247953.2 	Mouse DNA sequence from clone R...	40	10	
gi 51233561 gb AC110499.19 	Mus musculus chromosome 1, clon...	40	10	
gi 50902420 gb CP000003.1 	Streptococcus pyogenes MGAS10394...	40	10	
gi 50761406 ref XM_424720.1 	PREDICTED: Gallus gallus simil...	40	10	G
gi 21904646 gb AE014155.1 	Streptococcus pyogenes MGAS315, ...	40	10	
gi 34786898 emb AL831812.5 CNS08CAP	Oryza sativa chromosome...	40	10	
gi 21535755 emb AL713907.3 CNS07YQ7	Oryza sativa chromosome...	40	10	
gi 33620400 emb AL929018.14 	Mouse DNA sequence from clone ...	40	10	
gi 21281541 gb AC104163.2 	Homo sapiens chromosome 3 clone ...	40	10	
gi 21206336 gb AC100868.2 	Homo sapiens chromosome 8, clone...	40	10	
gi 27228874 gb AC093576.3 	Homo sapiens chromosome 1 clone ...	40	10	
gi 51534200 emb BX530059.4 	Zebrafish DNA sequence from clo...	40	10	
gi 21104611 dbj AP003241.3 	Oryza sativa (japonica cultivar...	40	10	
gi 15623809 dbj AP003231.3 	Oryza sativa (japonica cultivar...	40	10	
gi 25137544 dbj AP005900.1 	Homo sapiens genomic DNA, chrom...	40	10	
gi 46240964 gb AC145942.4 	Gallus gallus chromosome UNK clo...	40	10	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|16756377|gb|AC079238.7|](#) **D** Homo sapiens BAC clone RP11-719L21 from 4, complet
Length = 142462

Score = 1459 bits (736), Expect = 0.0
Identities = 750/752 (99%), Gaps = 2/752 (0%)
Strand = Plus / Plus

Query: 1 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
 |||
Sbjct: 128642 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 128701

Query: 61 cgacgagtattataacaagacacttgccacagagaataatactgctgccactcggaattc 120

```
|||||
Sbjct: 128702 cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 128761

Query: 121      tgatttcccagctctgggatgactataaaaagcagtgtagatgacttacagtattttctgat 180
|||||
Sbjct: 128762 tgatttcccagctctgggatgactataaaaagcagtgtagatgacttacagtattttctgat 128821

Query: 181      tgggctctatacatttgtaagtcttcttggtttatggggaatctacttattttaatggc 240
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Sbjct: 128822 tgggctctatacatttgtaagtcttcttggtttatggggaatctacttattttaatggc 128881

Query: 241      tctcatgaaaaagcgtaatcagaagactacggtaaaacttcctcataggcaatctggcctt 300
|||||
Sbjct: 128882 tctcatgaaaaagcgtaatcagaagactacggtaaaacttcctcataggcaatctggcctt 128941

Query: 301      ttctgatatcttggttgctgctgttttgctcacctttcacactgacgtctgtcttgctgga 360
|||||
Sbjct: 128942 ttctgatatcttggttgctgctgttttgctcacctttcacactgacgtctgtcttgctgga 129001

Query: 361      tcagtggtatgtttggcaaagtcagtgtgccatattatgccttttcttcaatgtgtgtcagt 420
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Sbjct: 129002 tcagtggtatgtttggcaaagtcagtgtgccatattatgccttttcttcaatgtgtgtcagt 129061

Query: 421      tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 480
|||||
Sbjct: 129062 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 129121

Query: 481      tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 540
|||||
Sbjct: 129122 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 129181

Query: 541      actaggttttgccatctgttctccccttcagtgtttcacagtcttgtggaacttcaaga 600
|||||
Sbjct: 129182 actaggttttgccatctgttctccccttcagtgtttcacagtcttgtggaacttcaaga 129241

Query: 601      aacatttggttcagcattgct-agcagcaggtatttatgtgttgagtcatggccatctga 659
|||||
Sbjct: 129242 aacatttggttcagcattgctgagcagcaggtatttatgtgttgagtcatggccatctga 129301

Query: 660      ttcatacagaattgcctttactatctctttattgctagttcagt-tattctgcccttagt 718
|||||
Sbjct: 129302 ttcatacagaattgcctttactatctctttattgctagttcagttatattctgcccttagt 129361

Query: 719      ttgtcttactgtaagtcatacaagtgctctgca 750
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Sbjct: 129362 ttgtcttactgtaagtcatacaagtgctctgca 129393
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Score = 505 bits (255), Expect = e-140
 Identities = 255/255 (100%)
 Strand = Plus / Plus

Query: 813 . agatctcgaagtgttttctacagactgaccatactgatattagtagtatttgcgtgttagttgg 872
 |||
 Sbjct: 129771 agatctcgaagtgttttctacagactgaccatactgatattagtagtatttgcgtgttagttgg 129830

Query: 873 atgccactacaccttttccatgtggtaactgattttaatgacaatcttatttcaaataagg 932
 |||
 Sbjct: 129831 atgccactacaccttttccatgtggtaactgattttaatgacaatcttatttcaaataagg 129890

Query: 933 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaaat 992
 |||
 Sbjct: 129891 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaaat 129950

Query: 993 ccaattctatatgggttttcttaataatgggattaaagctgatttagtgtcccttatacac 1052
 |||
 Sbjct: 129951 ccaattctatatgggttttcttaataatgggattaaagctgatttagtgtcccttatacac 130010

Query: 1053 tgtcttcatatgtaa 1067
 |||
 Sbjct: 130011 tgtcttcatatgtaa 130025

Score = 125 bits (63), Expect = 2e-25
 Identities = 63/63 (100%)
 Strand = Plus / Minus

Query: 750 atacgcctaaaaaggagaaacaacatgatggacaagatgagagacaataagtagcagggtcc 809
 |||
 Sbjct: 104166 atacgcctaaaaaggagaaacaacatgatggacaagatgagagacaataagtagcagggtcc 104107

Query: 810 agt 812
 |||
 Sbjct: 104106 agt 104104

☐ >gi|1438903|qb|U56079.1|HSU56079 **GU** Human Y5 receptor mRNA, complete cds
 Length = 1418

Score = 1459 bits (736), Expect = 0.0
 Identities = 750/752 (99%), Gaps = 2/752 (0%)
 Strand = Plus / Plus

Query: 1 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 60
 |||
 Sbjct: 10 ttttggttgctgacaaatgtctttttattccaagcaggactataatatggatttagagct 69

Query: 61 cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 120
|||||
Sbjct: 70 cgacgagtattataacaagacacttgccacagagaataataactgctgccactcggaattc 129

Query: 121 tgatttcccagctctgggatgactataaaaagcagtgtagatgacttacagtattttctgat 180
|||||
Sbjct: 130 tgatttcccagctctgggatgactataaaaagcagtgtagatgacttacagtattttctgat 189

Query: 181 tgggctctatacatttgtaagtccttcttggtttatggggaatctacttattttaatggc 240
|||||
Sbjct: 190 tgggctctatacatttgtaagtccttcttggtttatggggaatctacttattttaatggc 249

Query: 241 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 300
|||||
Sbjct: 250 tctcatgaaaaagcgtaatcagaagactacggtaaacttcctcataggcaatctggcctt 309

Query: 301 ttctgatatcttggttgctgttttgctcacctttcacactgacgtctgtcttgctgga 360
|||||
Sbjct: 310 ttctgatatcttggttgctgttttgctcacctttcacactgacgtctgtcttgctgga 369

Query: 361 tcagtggatgtttggcaaagtcagtgtgccatattatgccttttcttcaatgtgtgtcagt 420
|||||
Sbjct: 370 tcagtggatgtttggcaaagtcagtgtgccatattatgccttttcttcaatgtgtgtcagt 429

Query: 421 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 480
|||||
Sbjct: 430 tttggtttcaactttaattttaatatcaattgccattgtcaggtatcatatgataaaaca 489

Query: 481 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 540
|||||
Sbjct: 490 tcccatatctaataatttaacagcaaaccatggctactttctgatagctactgtctggac 549

Query: 541 actagggttttgccatctgttctccccttccagtgtttcacagtcttggtggaacttcaaga 600
|||||
Sbjct: 550 actagggttttgccatctgttctccccttccagtgtttcacagtcttggtggaacttcaaga 609

Query: 601 aacatttggttcagcattgct-agcagcaggtatttatgtgttgagtcatggccatctga 659
|||||
Sbjct: 610 aacatttggttcagcattgctgagcagcaggtatttatgtgttgagtcatggccatctga 669

Query: 660 ttcatacagaattgcctttactatctctttattgctagttcagt-tattctgcccttagt 718
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Sbjct: 670 ttcatacagaattgcctttactatctctttattgctagttcagtatattctgcccttagt 729

Query: 719 ttgtcttactgtaagtcatacaagtgctctgca 750
|||||
Sbjct: 730 ttgtcttactgtaagtcatacaagtgctctgca 761

Score = 505 bits (255), Expect = e-140
Identities = 255/255 (100%)
Strand = Plus / Plus

Query: 813 agatctcgaagtgttttctacagactgaccatactgatattagtagtatttgcgtgtagttgg 872
|||||
Sbjct: 1139 agatctcgaagtgttttctacagactgaccatactgatattagtagtatttgcgtgtagttgg 1198

Query: 873 atgccactacaccttttccatgtggtaactgattttaatgacaatcttatttcaaataagg 932
|||||
Sbjct: 1199 atgccactacaccttttccatgtggtaactgattttaatgacaatcttatttcaaataagg 1258

Query: 933 catttcaagttggtgtattgcatttgcatttgttgggcatgatgtcctgttgccttaata 992
|||||
Sbjct: 1259 catttcaagttggtgtattgcatttgcatttgttgggcatgatgtcctgttgccttaata 1318

Query: 993 ccaattctatatgggttttcttaataatgggattaaagctgatttagtgcccttatacac 1052
|||||
Sbjct: 1319 ccaattctatatgggttttcttaataatgggattaaagctgatttagtgcccttatacac 1378

Query: 1053 tgtcttcatatgtaa 1067
|||||
Sbjct: 1379 tgtcttcatatgtaa 1393

☐ >gi|1620655|gb|U66275.1|HSU66275 **GU** Human neuropeptide Y5 receptor (NPYR5) mRNA
Length = 1370

Score = 1402 bits (707), Expect = 0.0
Identities = 721/723 (99%), Gaps = 2/723 (0%)
Strand = Plus / Plus

Query: 30 ccaagcaggactataatatggatttagagctcgacgagtattataacaagacacttgcca 89
|||||
Sbjct: 1 ccaagcaggactataatatggatttagagctcgacgagtattataacaagacacttgcca 60

Query: 90 cagagaataatactgctgccactcggaattctgatttcccagctctgggatgactataaaa 149
|||||
Sbjct: 61 cagagaataatactgctgccactcggaattctgatttcccagctctgggatgactataaaa 120

Query: 150 gcagtgtagatgacttacagtattttctgattgggctctatacatttgtaagtcttcttg 209
|||||
Sbjct: 121 gcagtgtagatgacttacagtattttctgattgggctctatacatttgtaagtcttcttg 180

Query: 210 gctttatggggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagacta 269
|||||
Sbjct: 181 gctttatggggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagacta 240

Query: 270 cggtaaacttcctcataggcaatctggccttttctgatatcttggttgctgctgttttgct 329
|||||
Sbjct: 241 cggtaaacttcctcataggcaatctggccttttctgatatcttggttgctgctgttttgct 300

Query: 330 cacctttcacactgacgtctgtcttgctggatcagtggatggttggcaaagtcagtgtgcc 389
|||||
Sbjct: 301 cacctttcacactgacgtctgtcttgctggatcagtggatggttggcaaagtcagtgtgcc 360

Query: 390 atattatgccttttcttcaatgtgtgtcagtttgggttcaactttaattttaatatcaa 449
|||||
Sbjct: 361 atattatgccttttcttcaatgtgtgtcagtttgggttcaactttaattttaatatcaa 420

Query: 450 ttgccattgtcaggtatcatatgataaaacatcccatatctaataatttaacagcaaacc 509
|||||
Sbjct: 421 ttgccattgtcaggtatcatatgataaaacatcccatatctaataatttaacagcaaacc 480

Query: 510 atggctactttctgatagctactgtctggacactaggtttggccatctgttctccccttc 569
|||||
Sbjct: 481 atggctactttctgatagctactgtctggacactaggtttggccatctgttctccccttc 540

Query: 570 cagtgtttcacagtcttgtggaacttcaagaaacatttggttcagcattgct-agcagca 628
|||||
Sbjct: 541 cagtgtttcacagtcttgtggaacttcaagaaacatttggttcagcattgctgagcagca 600

Query: 629 ggtatttatgtgttgagtcatggccatctgattcatacagaattgcctttactatctctt 688
|||||
Sbjct: 601 ggtatttatgtgttgagtcatggccatctgattcatacagaattgcctttactatctctt 660

Query: 689 tattgctagttcagt-tattctgcccttagtttgtcttactgtaagtcatacaagtgct 747
|||||
Sbjct: 661 tattgctagttcagtatattctgcccttagtttgtcttactgtaagtcatacaagtgct 720

Query: 748 gca 750
|||
Sbjct: 721 gca 723

Score = 505 bits (255), Expect = e-140
Identities = 255/255 (100%)
Strand = Plus / Plus

Query: 813 agatctcgaagtgttttctacagactgaccatactgatattagtagttgctgtagttgg 872
|||||
Sbjct: 1101 agatctcgaagtgttttctacagactgaccatactgatattagtagttgctgtagttgg 1160

Query: 873 atgccactacaccttttccatgtggttaactgattttaatgacaatcttatttcaaatagg 932
|||||
Sbjct: 1161 atgccactacaccttttccatgtggttaactgattttaatgacaatcttatttcaaatagg 1220

Query: 933 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 992
 |||||
 Sbjct: 1221 catttcaagttggtgtattgcatttgtcatttgttgggcatgatgtcctgttgtcttaat 1280

Query: 993 ccaattctatatgggttttcttaataatgggattaaagctgatttagtgtcccttatacac 1052
 |||||
 Sbjct: 1281 ccaattctatatgggttttcttaataatgggattaaagctgatttagtgtcccttatacac 1340

Query: 1053 tgtcttcatatgtaa 1067
 |||||
 Sbjct: 1341 tgtcttcatatgtaa 1355

☐ >gi|22832895|gb|BC034224.1| **GU** Homo sapiens neuropeptide Y receptor Y5, mRNA (c
 IMAGE:4838926), partial cds
 Length = 3197

Score = 1386 bits (699), Expect = 0.0
 Identities = 713/715 (99%), Gaps = 2/715 (0%)
 Strand = Plus / Plus

Query: 38 gactataaatatggatttagagctcgacgagtattataacaagacacttgccacagagaat 97
 |||||
 Sbjct: 1514 gactataaatatggatttagagctcgacgagtattataacaagacacttgccacagagaat 1573

Query: 98 aatactgctgccactcggaattctgatttcccagctctgggatgactataaaaagcagtgtgta 157
 |||||
 Sbjct: 1574 aatactgctgccactcggaattctgatttcccagctctgggatgactataaaaagcagtgtgta 1633

Query: 158 gatgacttacagtattttctgattgggctctatacatttgtaagtcttcttggctttatg 217
 |||||
 Sbjct: 1634 gatgacttacagtattttctgattgggctctatacatttgtaagtcttcttggctttatg 1693

Query: 218 gggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagactacggtaaac 277
 |||||
 Sbjct: 1694 gggaatctacttattttaatggctctcatgaaaaagcgtaatcagaagactacggtaaac 1753

Query: 278 ttctcataggcaatctggccttttctgatatttgggtgtgctgttttgctcacctttc 337
 |||||
 Sbjct: 1754 ttctcataggcaatctggccttttctgatatttgggtgtgctgttttgctcacctttc 1813

Query: 338 aactgacgtctgtcttgctggatcagtggatgttggcaaagtcagtgtccatattatg 397
 |||||
 Sbjct: 1814 aactgacgtctgtcttgctggatcagtggatgttggcaaagtcagtgtccatattatg 1873

Query: 398 ccttttcttcaatgtgtgtcagtttgggttcaactttaattttaatatcaattgccatt 457
 |||||
 Sbjct: 1874 ccttttcttcaatgtgtgtcagtttgggttcaactttaattttaatatcaattgccatt 1933